

Epps, J.

1635 RUSH

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/155,676A

DATE: 04/22/2000  
TIME: 01:05:44

INPUT SET: S35359.raw

#13

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

1 SEQUENCE LISTING  
2  
3 (1) General Information:  
4  
5 (i) APPLICANT: WALLACH, David  
6 MALININ, Nikolai  
7 BOLDIN, Mark  
8 KOVALENKO, Andrei  
9 METT, Igor  
10  
11 (ii) TITLE OF INVENTION: MODULATORS OF TNF RECEPTOR ASSOCIATED  
12 FACTOR (TRAF), THEIR PREPARATION AND USE  
13  
14 (iii) NUMBER OF SEQUENCES: 20  
15  
16 (iv) CORRESPONDENCE ADDRESS:  
17 (A) ADDRESSEE: BROWDY AND NEIMAR, P.L.L.C.  
18 (B) STREET: 624 Ninth Street, N.W., Suite 300  
19 (C) CITY: Washington  
20 (D) STATE: D.C.  
21 (E) COUNTRY: USA  
22 (F) ZIP: 20001  
23  
24 (v) COMPUTER READABLE FORM:  
25 (A) MEDIUM TYPE: Floppy disk  
26 (B) COMPUTER: IBM PC compatible  
27 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
28 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
29  
30 (vi) CURRENT APPLICATION DATA:  
31 (A) APPLICATION NUMBER: US 09/155,676  
32 (B) FILING DATE: 04-JAN-1999  
33 (C) CLASSIFICATION:  
34  
35 (vii) PRIOR APPLICATION DATA:  
36 (A) APPLICATION NUMBER: PCT/IL97/00117  
37 (B) FILING DATE: 01-APR-1997  
38  
39 (vii) PRIOR APPLICATION DATA:  
40 (A) APPLICATION NUMBER: IL 117800  
41 (B) FILING DATE: 02-APR-1996  
42  
43 (vii) PRIOR APPLICATION DATA:  
44 (A) APPLICATION NUMBER: IL 119133  
45 (B) FILING DATE: 26-AUG-1996  
46

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PATENT APPLICATION US/09/155,676ADATE: 04/22/2000  
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47 (viii) ATTORNEY/AGENT INFORMATION:  
48 (A) NAME: BROWDY, Roger L.  
49 (B) REGISTRATION NUMBER: 25,618  
50 (C) REFERENCE/DOCKET NUMBER: WALLACH=21

51  
52 (ix) TELECOMMUNICATION INFORMATION:  
53 (A) TELEPHONE: 202-628-5197  
54 (B) TELEFAX: 202-737-3528

55

56  
57 (2) INFORMATION FOR SEQ ID NO: 1:  
58

59 (i) SEQUENCE CHARACTERISTICS:  
60 (A) LENGTH: 1906 base pairs  
61 (B) TYPE: nucleic acid  
62 (C) STRANDEDNESS: single  
63 (D) TOPOLOGY: linear

64  
65 (ii) MOLECULE TYPE: cDNA

66  
67 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

68  
69 CATTGGGTCA CGCGGTGGCG GCGCTCTAGA ATAGTGGATC CCCCCGGCTG CAGGAATTG 60  
70  
71 ATTGAGGCC ACGAACGGCCG GCGGCGCGGC GCANGCACCG GCCCCGGGAN AGGCNCCATG 120  
72  
73 AGCGGATCNC NGAACNATGA CAAAAGACAA TTTCTGCTGG AGCGACTGCT GGATGCAGTG 180  
74  
75 AAACAGTGCC AGATCCGCTT TNGAGGGAGA AAGGAGATTG CCTCGGATTC CGACAGCAGG 240  
76  
77 GTCACCTGTC TGTGTGCCA GTTGAAGCC GTCCTGCAGC ATGGCTTGAA GAGGAGTCGA 300  
78  
79 GGATTGGCAC TCACAGCGGC AGCGATCAAG CAGGCAGCGG GCTTGCCAG CAAAACCGAA 360  
80  
81 ACAGAGCCCG TGTCTGGTA CTACGTGAAG GAGGTCCCTCA ACAAGCACGA GCTGCAGCGC 420  
82  
83 TTCTACTCCC TGCGCCACAT CGCCTCAGAC GTGGGCCGGG GTCGCGCCTG GCTGCGCTGT 480  
84  
85 GCCCTCAACG AACACTCCCT GGAGCGCTAC CTGCACATGC TCCTGGCCGA CCGCTGCAGG 540  
86  
87 CTGAGCACCT TTTATGAAGA CTGGTCTTT GTGATGGATG AAGAAAGGTC CAGTATGCTT 600  
88  
89 CCTACCATGG CAGCAGGTCT GAACTCCATA CTCTTGCAGA TTAACATCGA CAACAAGGAT 660  
90  
91 TTGAACGGGC AGAGTAAGTT TGCTCCACC GTTTCAGACC TCTTAAAGGA GTCAACGCAG 720  
92  
93 AACGTGACCT CCTTGCTGAA GGAGTCCACG CAAGGAGTGA GCAGCCTGTT CAGGGAGATC 780  
94  
95 ACAGCCTCCT CTGCCGTCTC CATCCTCATC AAACCTGAAC AGGAGACCGA CCCTTGCCCTG 840  
96  
97 TCGTGTCCAG GAATGTCAGT GCTGATGCCA AATGCAAAAA GGAGCGGAAG AAGAAAAAGA 900  
98  
99 AAGTGACCAA CATAATCTCA TTTGATGATG AGGAAGATGA GCAGAACTCT GGGGACGTGT 960

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100 TTAAAAAGAC ACCTGGGGCA GGGGAGAGCT CAGAGGACAA CTCCGACCGC TCCTCTGTCA 1020  
101  
102 ATATCATGTC CGCCTTGAA AGCCCTTCG GGCTAACTC CAATGGAATC AGAGCAGCAA 1080  
103  
104 CTCATGGAAA ATTGATTCCC TGTCTTGAA CGGGGAGTTT GGGTACCAGA AGCTTGATGT 1140  
105  
106 GAAAAGCATC GATGATGAAG ATGTGGATGA AAACGAAGAT GACGTGTATG GAAACTCATC 1200  
107  
108 AGGAAGGAAG CACAGGGGCC ACTCGGAGTC GCCCGAGAAG CCACTGGAAG GGAACACCTG 1260  
109  
110 CCTCTCCCAG ATGCACAGCT GGGCTCCGCT GAAGGTGCTG CACAATGACT CCGACATCCT 1320  
111  
112 CTTCCCTGTC AGTGGCGTGG GCTCCTACAG CCCAGCAGAT GCCCCCCCTCG GAAGCCTGGA 1380  
113  
114 GAACGGGACA GGACCAGAGG ACCACGTTCT CCCGGATCCT GGACTTCGGT ACAGTGTGGA 1440  
115  
116 AGCCAGCTCT CCAGGCCACG GAAGTCCTCT GAGCAGCCTG TTACTTCTGC CTCAGTGCCA 1500  
117  
118 GAGTCCATGA CAATTAGTGA ACTGCGCCAG GCCACTGTGG CCATGATGAA CAGGAAGGAT 1560  
119  
120 GAGCTGGAGG AGGAGAACAG ATCACTGCGA AACCTGCTCG ACGGTGAGAT GGAGCACTCA 1620  
121  
122 GCCGCGCTCC GGCAAGAGGT GGACACCTTG AAAAGGAAGG TGGCTGAACA GGAGGAGCGG 1680  
123  
124 CAGGGCATGA AGGTCCAGGC GCTGCCAGC TATCTTGCT ATTTTGAG GAGATTCTAA 1740  
125  
126 CCCCCACGTGA GAACCATGTG GTGGAGAAAT GGAGGGAGAG AGAAATCCAA CAGTTCCCTGA 1800  
127  
128 TAGTCTCATT TGAGCTCCTG GATCCAGTCT TTCCTGAAGC TGTGTTCCCT CTGGACTTTT 1860  
129  
130 CATGTATGTG AGCCAATAAA TTGCTTCAT TCCTTGAAAA AAAAAAA 1906  
131  
132 (2) INFORMATION FOR SEQ ID NO: 2:  
133  
134 (i) SEQUENCE CHARACTERISTICS:  
135 (A) LENGTH: 604 amino acids  
136 (B) TYPE: amino acid  
137 (C) STRANDEDNESS: single  
138 (D) TOPOLOGY: linear  
139  
140 (ii) MOLECULE TYPE: protein  
141  
142 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:  
143  
144 Xaa Thr Gly Pro Gly Xaa Gly Xaa Met Ser Gly Ser Xaa Asn Xaa Asp  
145 1 5 10 15  
146  
147 Lys Arg Gln Phe Leu Leu Glu Arg Leu Leu Asp Ala Val Lys Gln Cys  
148 20 25 30  
149  
150 Gln Ile Arg Phe Xaa Gly Arg Lys Glu Ile Ala Ser Asp Ser Asp Ser  
151 35 40 45  
152

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153  
154 Arg Val Thr Cys Leu Cys Ala Gln Phe Glu Ala Val Leu Gln His Gly  
155 50 55 60  
156  
157 Leu Lys Arg Ser Arg Gly Leu Ala Leu Thr Ala Ala Ala Ile Lys Gln  
158 65 70 75 80  
159  
160 Ala Ala Gly Phe Ala Ser Lys Thr Glu Thr Glu Pro Val Phe Trp Tyr  
161 85 90 95  
162  
163 Tyr Val Lys Glu Val Leu Asn Lys His Glu Leu Gln Arg Phe Tyr Ser  
164 100 105 110  
165  
166 Leu Arg His Ile Ala Ser Asp Val Gly Arg Gly Arg Ala Trp Leu Arg  
167 115 120 125  
168  
169 Cys Ala Leu Asn Glu His Ser Leu Glu Arg Tyr Leu His Met Leu Leu  
170 130 135 140  
171  
172 Ala Asp Arg Cys Arg Leu Ser Thr Phe Tyr Glu Asp Trp Ser Phe Val  
173 145 150 155 160  
174  
175 Met Asp Glu Glu Arg Ser Ser Met Leu Pro Thr Met Ala Ala Gly Leu  
176 165 170 175  
177  
178 Asn Ser Ile Leu Phe Ala Ile Asn Ile Asp Asn Lys Asp Leu Asn Gly  
179 180 185 190  
180  
181 Gln Ser Lys Phe Ala Pro Thr Val Ser Asp Leu Leu Lys Glu Ser Thr  
182 195 200 205  
183  
184 Gln Asn Val Thr Ser Leu Leu Lys Glu Ser Thr Gln Gly Val Ser Ser  
185 210 215 220  
186  
187 Leu Phe Arg Glu Ile Thr Ala Ser Ser Ala Val Ser Ile Leu Ile Lys  
188 225 230 235 240  
189  
190 Pro Glu Gln Glu Thr Asp Pro Cys Leu Ser Cys Pro Gly Met Ser Val  
191 245 250 255  
192  
193 Leu Met Pro Asn Ala Lys Arg Ser Gly Arg Arg Lys Arg Lys Xaa Pro  
194 260 265 270  
195  
196 Thr Xaa Ser His Leu Met Met Arg Lys Met Ser Arg Thr Leu Gly Thr  
197 275 280 285  
198  
199 Cys Leu Lys Arg His Leu Gly Gln Gly Arg Ala Gln Arg Thr Thr Pro  
200 290 295 300  
201  
202 Thr Ala Pro Leu Ser Ile Ser Cys Pro Pro Leu Lys Ala Pro Ser Gly  
203 305 310 315 320  
204  
205 Leu Thr Pro Met Glu Ser Glu Gln Gln Leu Met Glu Asn Xaa Phe Pro

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	325	330	335
206			
207			
208	Val Phe Glu Arg Gly Val Trp Val Pro Glu Ala Xaa Cys Glu Lys His		
209	340	345	350
210			
211	Arg Xaa Xaa Arg Cys Gly Xaa Lys Arg Arg Xaa Arg Val Trp Lys Leu		
212	355	360	365
213			
214	Ile Arg Lys Glu Ala Gln Gly Pro Leu Gly Val Ala Arg Glu Ala Thr		
215	370	375	380
216			
217	Gly Arg Glu His Leu Pro Leu Pro Asp Ala Gln Leu Gly Ser Ala Glu		
218	385	390	395
219			
220	Gly Ala Ala Gln Xaa Leu Arg His Pro Leu Pro Cys Gln Trp Arg Gly		
221	405	410	415
222			
223	Leu Leu Gln Pro Ser Arg Cys Pro Pro Arg Lys Pro Gly Glu Arg Asp		
224	420	425	430
225			
226	Arg Thr Arg Gly Pro Arg Ser Pro Gly Ser Trp Thr Ser Val Gln Cys		
227	435	440	445
228			
229	Gly Ser Gln Leu Ser Arg Pro Arg Lys Ser Ser Glu Gln Pro Val Thr		
230	450	455	460
231			
232	Ser Ala Ser Val Pro Glu Ser Met Thr Ile Ser Glu Leu Arg Gln Ala		
233	465	470	475
234			
235	Arg Thr Val Ala Met Met Asn Arg Lys Asp Glu Leu Glu Glu Asn Arg		
236	485	490	495
237			
238	Ser Leu Arg Asn Leu Leu Asp Gly Glu Met Glu His Ser Ala Ala Leu		
239	500	505	510
240			
241	Arg Gln Glu Val Asp Thr Leu Lys Arg Lys Val Ala Glu Gln Glu Glu		
242	515	520	525
243			
244	Arg Gln Gly Met Lys Val Gln Ala Leu Ala Ser Tyr Leu Cys Tyr Phe		
245	530	535	540
246			
247	Val Arg Arg Phe Xaa Pro His Val Arg Thr Met Trp Trp Arg Asn Gly		
248	545	550	555
249			
250	Gly Arg Glu Lys Ser Asn Ser Ser Xaa Xaa Ser His Leu Ser Ser Trp		
251	565	570	575
252			
253	Ile Gln Ser Phe Leu Lys Leu Cys Phe Leu Trp Thr Phe His Val Cys		
254	580	585	590
255			
256	Glu Pro Ile Asn Cys Phe His Ser Leu Lys Lys Lys		
257	595	600	
258			

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**SEQUENCE VERIFICATION REPORT**  
**PATENT APPLICATION US/09/155,676A**

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